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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/965,175

DATE: 10/16/2001

TIME: 15:38:11

Input Set : A:\PhzO.ST25.txt

Output Set: N:\CRF3\10162001\I965175.raw

3 <110> APPLICANT: Thomashow, Linda S.  
4 Delaney, Shannon M.  
5 Mavrodi, Dmitri V.  
6 Weller, David M.  
8 <120> TITLE OF INVENTION: Sequences Encoding PhzO and Methods  
10 <130> FILE REFERENCE: 0229.99  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/965,175  
C--> 12 <141> CURRENT FILING DATE: 2001-09-27  
12 <150> PRIOR APPLICATION NUMBER: US 60/236,634  
13 <151> PRIOR FILING DATE: 2000-09-29  
15 <160> NUMBER OF SEQ ID NOS: 11  
17 <170> SOFTWARE: PatentIn version 3.1  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 2869  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Pseudomonas chlororaphis  
24 <220> FEATURE:  
25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (89)..(1564)  
27 <223> OTHER INFORMATION:  
30 <220> FEATURE:  
31 <221> NAME/KEY: gene  
32 <222> LOCATION: (76)..(1564)  
33 <223> OTHER INFORMATION:  
36 <220> FEATURE:  
37 <221> NAME/KEY: RBS  
38 <222> LOCATION: (76)..(81)  
39 <223> OTHER INFORMATION:  
42 <400> SEQUENCE: 1  
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45 aaagtcagac attactgagg ctgctacc atg cta gat ttt caa aac aag cgt 112  
46 Met Leu Asp Phe Gln Asn Lys Arg  
47 1 5  
49 aaa tat ctg aaa agt gca gaa tcc ttc aaa gct tca ctg cgt gat aac 160  
50 Lys Tyr Leu Lys Ser Ala Glu Ser Phe Lys Ala Ser Leu Arg Asp Asn  
51 10 15 20  
53 cgc act gtt att tat caa ggc caa gtt gtt gag gat gtg act aca cac 208  
54 Arg Thr Val Ile Tyr Gln Gly Gln Val Val Glu Asp Val Thr Thr His  
55 25 30 35 40  
57 ttc tct acg gct gga ggc ata tcg caa gtt gca gaa atc tac gaa gaa 256  
58 Phe Ser Thr Ala Gly Gly Ile Ser Gln Val Ala Glu Ile Tyr Glu Glu  
59 45 50 55  
61 caa ttc agc ggt gaa cac gac gac att ctg act tac gta cgc ccc gac 304  
62 Gln Phe Ser Gly Glu His Asp Asp Ile Leu Thr Tyr Val Arg Pro Asp  
63 60 65 70  
65 ggt tac ctg gcc tct tct gcc tat atg ccc cct aga aac aaa gaa gac 352  
66 Gly Tyr Leu Ala Ser Ser Ala Tyr Met Pro Pro Arg Asn Lys Glu Asp

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67	75	80	85	
69	ttg gcg tcg cga cgc cgc gca atc atg tac gtc tcg caa aaa acc tgg	400		
70	Leu Ala Ser Arg Arg Arg Ala Ile Met Tyr Val Ser Gln Lys Thr Trp			
71	90	95	100	
73	ggc acc cac tgc cgt aac ctg gac atg atc gcc agc ttc acc gtc ggc	448		
74	Gly Thr His Cys Arg Asn Leu Asp Met Ile Ala Ser Phe Thr Val Gly			
75	105	110	115	120
77	atg atg gga tat ctg ccg aca ttc agg aaa aaa tgc cct gag tac gca	496		
78	Met Met Gly Tyr Leu Pro Thr Phe Arg Lys Lys Cys Pro Glu Tyr Ala			
79	125	130	135	
81	gaa aac att acc gaa tac cat gac tac gcc gag cgc aac agc ctg tat	544		
82	Glu Asn Ile Thr Glu Tyr His Asp Tyr Ala Glu Arg Asn Ser Leu Tyr			
83	140	145	150	
85	ttg tct gag acc att gtt gat cca cag ggc tat cgg gca cgt acc cac	592		
86	Leu Ser Glu Thr Ile Val Asp Pro Gln Gly Tyr Arg Ala Arg Thr His			
87	155	160	165	
89	ggc acc gac ctc aac ctg ccg ccg ccc gat cgt gcc gtg atg agg atc	640		
90	Gly Thr Asp Leu Asn Leu Pro Pro Pro Asp Arg Ala Val Met Arg Ile			
91	170	175	180	
93	aac aag cag aac gcc gag ggc atc tgg atc agc ggc gtc aaa ggc gtg	688		
94	Asn Lys Gln Asn Ala Glu Gly Ile Trp Ile Ser Gly Val Lys Gly Val			
95	185	190	195	200
97	ggc acg gca gca ccg cag tcc aat gaa ata ttt gtt ggc agc ttg ttc	736		
98	Gly Thr Ala Ala Pro Gln Ser Asn Glu Ile Phe Val Gly Ser Leu Phe			
99	205	210	215	
101	ccc gca gcg ccc gag gag tca ttc tgg gct tac gtc cct gtc gat gcg	784		
102	Pro Ala Ala Pro Glu Glu Ser Phe Trp Ala Tyr Val Pro Val Asp Ala			
103	220	225	230	
105	ccg ggg gtg aag att ttt tgc cga gag att gtc tcc cag cct cac gcc	832		
106	Pro Gly Val Lys Ile Phe Cys Arg Glu Ile Val Ser Gln Pro His Ala			
107	235	240	245	
109	agc gcc tat gac cac ccg ctc ata tcc aaa ggt gaa gaa gcc gag gcg	880		
110	Ser Ala Tyr Asp His Pro Leu Ile Ser Lys Gly Glu Glu Ala Glu Ala			
111	250	255	260	
113	atg gtg gta ttc gat aac gtg ttc att cca cgc tgg cga atc atg gcg	928		
114	Met Val Val Phe Asp Asn Val Phe Ile Pro Arg Trp Arg Ile Met Ala			
115	265	270	275	280
117	gcg aac gtg ccg gaa ctg gcc agc gcc ggc ttc ttc agt ctg tgg acc	976		
118	Ala Asn Val Pro Glu Leu Ala Ser Ala Gly Phe Phe Ser Leu Trp Thr			
119	285	290	295	
121	tca tac agc cat tgg tac acg ctc gtg cgc ctg gaa acc aag gct gac	1024		
122	Ser Tyr Ser His Trp Tyr Thr Leu Val Arg Leu Glu Thr Lys Ala Asp			
123	300	305	310	
125	ctg tat gcc gga ctg gcc aag gtg atc atg gaa gtc ctg ggc ctt gag	1072		
126	Leu Tyr Ala Gly Leu Ala Lys Val Ile Met Glu Val Leu Gly Leu Glu			
127	315	320	325	
129	ggg att gcg gtg gtt cgc cag cgg gtc agc gaa ata gtg cag ctt gcg	1120		
130	Gly Ile Ala Val Val Arg Gln Arg Val Ser Glu Ile Val Gln Leu Ala			
131	330	335	340	

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133 gaa ata ctc aaa ggc atg tgc atc gcc tcc atc gaa acg gcc gag atg      1168
134 Glu Ile Leu Lys Gly Met Cys Ile Ala Ser Ile Glu Thr Ala Glu Met
135 345                      350                      355                      360
137 tcc gac ggc gac ata ttg ctg cct ggc cac aac gca ctg gcc gcc gga      1216
138 Ser Asp Gly Asp Ile Leu Leu Pro Gly His Asn Ala Leu Ala Ala Gly
139                      365                      370                      375
141 agg gtt ttt gcc atg gag aaa ttg cct cgg gtg ctg cat ttg ctc aga      1264
142 Arg Val Phe Ala Met Glu Lys Leu Pro Arg Val Leu His Leu Leu Arg
143                      380                      385                      390
145 gag ctg tgc gga cag ggc ttg atc ctc agg ttc aac gag aaa gac ttg      1312
146 Glu Leu Cys Gly Gln Gly Leu Ile Leu Arg Phe Asn Glu Lys Asp Leu
147                      395                      400                      405
149 gcc gcc gac gcc gcc ttt ggc cag aag ttc tcc tgg ttt ctt gac acg      1360
150 Ala Ala Asp Ala Ala Phe Gly Gln Lys Phe Ser Trp Phe Leu Asp Thr
151                      410                      415                      420
153 caa agc gtg ggc gcc aga gag aag aac ctg ctg atg aac cta gtg tgg      1408
154 Gln Ser Val Gly Ala Arg Glu Lys Asn Leu Leu Met Asn Leu Val Trp
155 425                      430                      435                      440
157 gac gtg gct gcc agt gag cac tcc aca cgt gca ttg gtg ttt gaa gaa      1456
158 Asp Val Ala Ala Ser Glu His Ser Thr Arg Ala Leu Val Phe Glu Glu
159                      445                      450                      455
161 cag cac gca ctc agc gag ccc ctg ctg cgc gat aac ctg gtg ctg gac      1504
162 Gln His Ala Leu Ser Glu Pro Leu Leu Arg Asp Asn Leu Val Leu Asp
163                      460                      465                      470
165 tac gac tac cgc gaa agc aca agc ctg ata cgc cgc cta gtg ggg ctc      1552
166 Tyr Asp Tyr Arg Glu Ser Thr Ser Leu Ile Arg Arg Leu Val Gly Leu
167                      475                      480                      485
169 aac gcc aaa tag acctgattgc cgtgtaggcg ccgcgcgaacc cttcattcgt      1604
170 Asn Ala Lys
171                      490
173 gccgactgaa ctcggcacga atgaaggggtt gtccgcctcc ggccccaggc atcccgtaa      1664
175 cttccaacct tcaacggtag tacaccgccc cattagcatc caaatgaata cggcaggagc      1724
177 ccgttacagc gctggcgctg gatgcctggc tacgcttgca caggatctcg gtccgagacg      1784
179 agccagggtt accggccccc ctttgttcga gccatgccac ttggcaggct cgttcagttg      1844
181 tagcggtcag cctgtcgccg gttggcttgc caccggtacc gaacgtcagt agggcgcttg      1904
183 gtccgggttg catccgggaa tgcagtgaaa cgcgtcgctt ggttccaggc ccaggcgcca      1964
185 gccaacggag aaaacaaggc gctcaccagc gcccatgcac acaggcgcgc cgcgctttca      2024
187 ataccaaaag ccaagccccg tcacagcccc ccaagcgcca cctccaggcc agcgtccagc      2084
189 atcggccctc gccagaagc gccagccata tcggcaccgt agcgaccagc gaaagggta      2144
191 gcatgggccc gctcaactgt gtacattcct cccacggac gacacatcat ttaccagtg      2204
193 aacggagtgc aacgcgtgtt ctcgaccctc aatccgcgtc accgcccggc tgccagtttc      2264
195 tcgttgctag ccgtggcctt aagcctcgcc gcctgcaacg cttccgcccc ttcccatacc      2324
197 gccctgcccc ccgccccgga aatcgcttggt gggttatcgca ccgacctgca agtgacgac      2384
199 gccgaccggc atatggcggc cgcggccaac ccgttgcgcg ccgaagccgg gcgcgaaatg      2444
201 ttgcgcaagg gtggttcggc catcgatgcg gcgattgcca tgcaagcggt gctgaccctg      2504
203 gtggagccgc agtcgtcggg gatcgcgggc ggcgccctga tcgtgctctg ggacggcaag      2564
205 gcggtgcgca cgtacgacgg tcgcgaaacc gcgcggcgcc gggccaccga aaagttgttc      2624
207 ctgcaagccg acggcaagcc catgccgttc ccccgggcac agatcggcgg ccgttcgggtg      2684
209 ggtacgcccc gcgtgctgcg cgccctggaa ctggccccatg aaaaacacgg ccgcctgccc      2744

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211 tgggcgcagc tggtcgagcc ggcgattcgc ctggcggacc aggggtttccc gatctccccg 2804
213 cgcctgcaca gcatgataaa aaccgatccg tacctggcga aatcgccgga tatggccgcc 2864
215 tacttt 2869
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219 <211> LENGTH: 491
220 <212> TYPE: PRT
221 <213> ORGANISM: Pseudomonas chlororaphis
223 <400> SEQUENCE: 2
225 Met Leu Asp Phe Gln Asn Lys Arg Lys Tyr Leu Lys Ser Ala Glu Ser
226 1 5 10 15
229 Phe Lys Ala Ser Leu Arg Asp Asn Arg Thr Val Ile Tyr Gln Gly Gln
230 20 25 30
233 Val Val Glu Asp Val Thr Thr His Phe Ser Thr Ala Gly Gly Ile Ser
234 35 40 45
237 Gln Val Ala Glu Ile Tyr Glu Glu Gln Phe Ser Gly Glu His Asp Asp
238 50 55 60
241 Ile Leu Thr Tyr Val Arg Pro Asp Gly Tyr Leu Ala Ser Ser Ala Tyr
242 65 70 75 80
245 Met Pro Pro Arg Asn Lys Glu Asp Leu Ala Ser Arg Arg Arg Ala Ile
246 85 90 95
249 Met Tyr Val Ser Gln Lys Thr Trp Gly Thr His Cys Arg Asn Leu Asp
250 100 105 110
253 Met Ile Ala Ser Phe Thr Val Gly Met Met Gly Tyr Leu Pro Thr Phe
254 115 120 125
257 Arg Lys Lys Cys Pro Glu Tyr Ala Glu Asn Ile Thr Glu Tyr His Asp
258 130 135 140
261 Tyr Ala Glu Arg Asn Ser Leu Tyr Leu Ser Glu Thr Ile Val Asp Pro
262 145 150 155 160
265 Gln Gly Tyr Arg Ala Arg Thr His Gly Thr Asp Leu Asn Leu Pro Pro
266 165 170 175
269 Pro Asp Arg Ala Val Met Arg Ile Asn Lys Gln Asn Ala Glu Gly Ile
270 180 185 190
273 Trp Ile Ser Gly Val Lys Gly Val Gly Thr Ala Ala Pro Gln Ser Asn
274 195 200 205
277 Glu Ile Phe Val Gly Ser Leu Phe Pro Ala Ala Pro Glu Glu Ser Phe
278 210 215 220
281 Trp Ala Tyr Val Pro Val Asp Ala Pro Gly Val Lys Ile Phe Cys Arg
282 225 230 235 240
285 Glu Ile Val Ser Gln Pro His Ala Ser Ala Tyr Asp His Pro Leu Ile
286 245 250 255
289 Ser Lys Gly Glu Glu Ala Glu Ala Met Val Val Phe Asp Asn Val Phe
290 260 265 270
293 Ile Pro Arg Trp Arg Ile Met Ala Ala Asn Val Pro Glu Leu Ala Ser
294 275 280 285
297 Ala Gly Phe Phe Ser Leu Trp Thr Ser Tyr Ser His Trp Tyr Thr Leu
298 290 295 300
301 Val Arg Leu Glu Thr Lys Ala Asp Leu Tyr Ala Gly Leu Ala Lys Val
302 305 310 315 320
305 Ile Met Glu Val Leu Gly Leu Glu Gly Ile Ala Val Val Arg Gln Arg

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306          325          330          335
309 Val Ser Glu Ile Val Gln Leu Ala Glu Ile Leu Lys Gly Met Cys Ile
310          340          345          350
313 Ala Ser Ile Glu Thr Ala Glu Met Ser Asp Gly Asp Ile Leu Leu Pro
314          355          360          365
317 Gly His Asn Ala Leu Ala Ala Gly Arg Val Phe Ala Met Glu Lys Leu
318          370          375          380
321 Pro Arg Val Leu His Leu Leu Arg Glu Leu Cys Gly Gln Gly Leu Ile
322 385          390          395          400
325 Leu Arg Phe Asn Glu Lys Asp Leu Ala Ala Asp Ala Ala Phe Gly Gln
326          405          410          415
329 Lys Phe Ser Trp Phe Leu Asp Thr Gln Ser Val Gly Ala Arg Glu Lys
330          420          425          430
333 Asn Leu Leu Met Asn Leu Val Trp Asp Val Ala Ala Ser Glu His Ser
334          435          440          445
337 Thr Arg Ala Leu Val Phe Glu Glu Gln His Ala Leu Ser Glu Pro Leu
338          450          455          460
341 Leu Arg Asp Asn Leu Val Leu Asp Tyr Asp Tyr Arg Glu Ser Thr Ser
342 465          470          475          480
345 Leu Ile Arg Arg Leu Val Gly Leu Asn Ala Lys
346          485          490

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349 &lt;210&gt; SEQ ID NO: 3

350 &lt;211&gt; LENGTH: 20

351 &lt;212&gt; TYPE: DNA

352 &lt;213&gt; ORGANISM: artificial sequence

354 &lt;220&gt; FEATURE:

355 &lt;223&gt; OTHER INFORMATION: primer PCA2a

357 &lt;400&gt; SEQUENCE: 3

358 ttgccaagcc tcgctccaac

20

361 &lt;210&gt; SEQ ID NO: 4

362 &lt;211&gt; LENGTH: 20

363 &lt;212&gt; TYPE: DNA

364 &lt;213&gt; ORGANISM: artificial sequence

366 &lt;220&gt; FEATURE:

367 &lt;223&gt; OTHER INFORMATION: primer PCA3b

369 &lt;400&gt; SEQUENCE: 4

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20

373 &lt;210&gt; SEQ ID NO: 5

374 &lt;211&gt; LENGTH: 21

375 &lt;212&gt; TYPE: DNA

376 &lt;213&gt; ORGANISM: artificial sequence

378 &lt;220&gt; FEATURE:

379 &lt;223&gt; OTHER INFORMATION: primer 30-84XBA

381 &lt;400&gt; SEQUENCE: 5

382 aagtcagat gcgaaagaac g

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385 &lt;210&gt; SEQ ID NO: 6

386 &lt;211&gt; LENGTH: 21

387 &lt;212&gt; TYPE: DNA

388 &lt;213&gt; ORGANISM: artificial sequence

VERIFICATION SUMMARY

DATE: 10/16/2001

PATENT APPLICATION: US/09/965,175

TIME: 15:38:12

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Output Set: N:\CRF3\10162001\I965175.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date